

1 MELALCRWG LLLALLPBG A STQVCTGTD MKLRLPASPE THLDMLRHL Y QGCQVVGNL ELTYLPTNAS LSFLODIOEV QGYVLIAHNQ VRQVPLQRLR  
101 IVRGTOFLFED NYALAVLDNG DPLNNTTPTVT GASPGGLREL QLRSLTEILK GGVLIQRNPQ LCVQDTILMK DIFHKNNOLA LTLIDTNRSR ACHPCSPMCK  
201 GSRCWGESSE DCQSLTRTVC AGGCARCKGP LPTDCHEQC AAGCTGPKHS DCLACLHFNH SGICELHCPA LVTYNTDTFE SMPNPEGRYT FGASCVTACP  
301 YNYLSTDVGS CTIVCPHLNQ EVTAEDGTQR CEKCSKPCAR VCYGLGMEHL REVRAVTSAN IQEFAGCKKI FGSIAFLPES FDGDPAASNTA PLQPEQLQVF  
401 ETLEEITGYL YISAMPDSL P DLSEFQNLQV IRGRILHNGA YSLTLQGLGI SWLGLRSLRE LSGSLALIH NHLCFVHTV PWDQLFRNPH QALLHTANRP  
501 EDECVGEGLA CHQLCARGHC WGPPTQCVN CSQFLRGQEC VEECRVLQGL PREYVNAHHC LPCHPECQPO NGSVTCFGRPE ADQCVACAHY KDPFPCVARC  
601 PSGVKPDL SY MPIWKFPDEE GACQPCPINC THSCVDLDDK GCPAE (SEQ ID NO: 13)

Fig. 1A

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00E290"00820960

7C2 aa 22-53 (31 residues)  
7F3 aa 22-53 (31 residues)  
2C4 aa 22-584 (562 residues)  
7D3 aa 22-584 (562 residues)  
3E8 aa 512-625 (113 residues)  
4D5 aa 529-625 (96 residues)  
2H11 aa 529-645 (116 residues)  
3H4 aa 541-599 (58 residues)

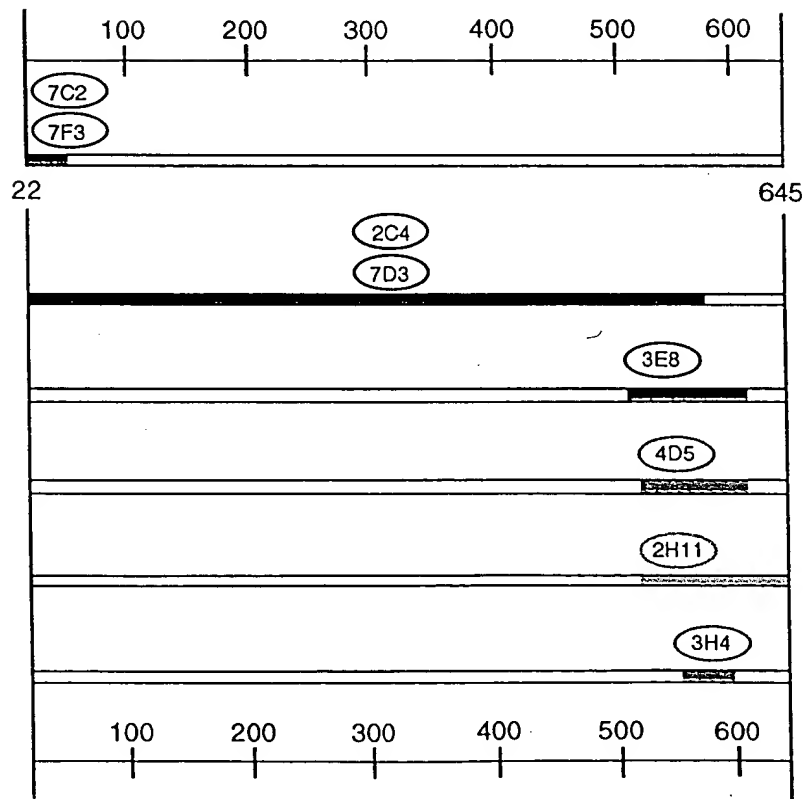


Fig. 1B

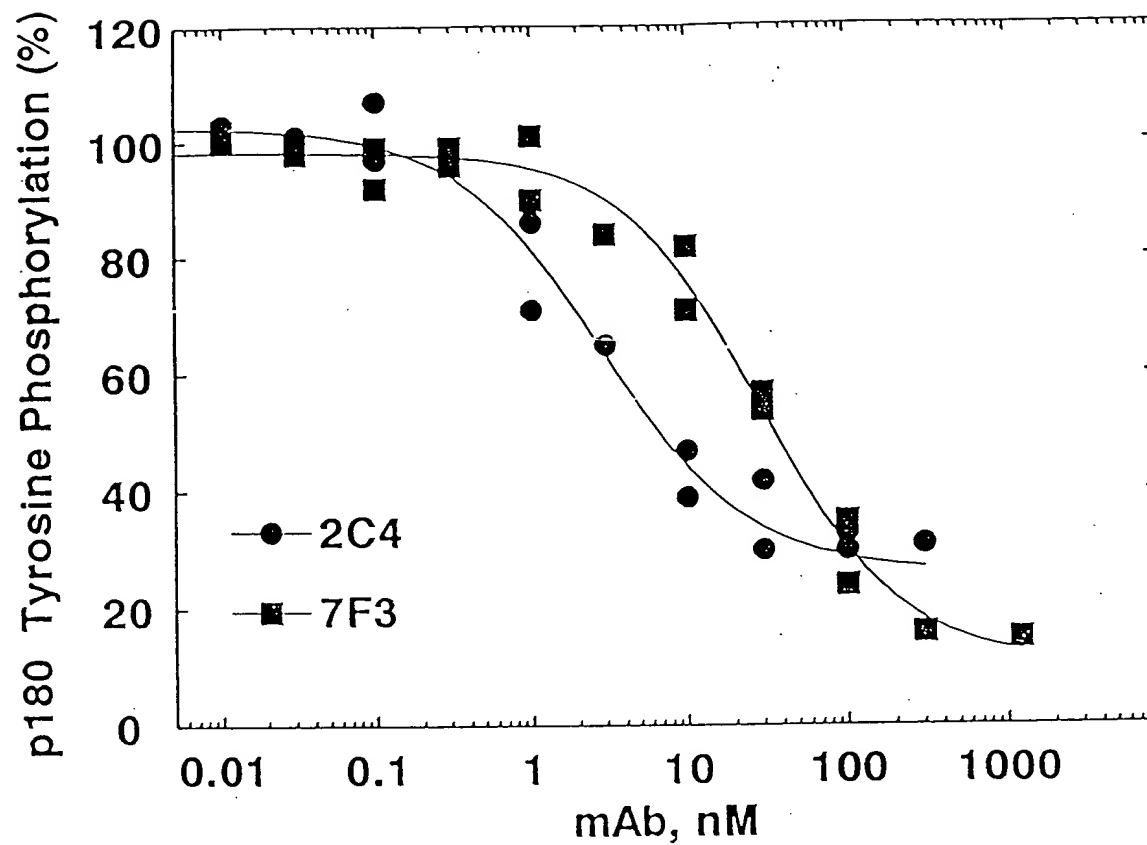


Fig. 2A

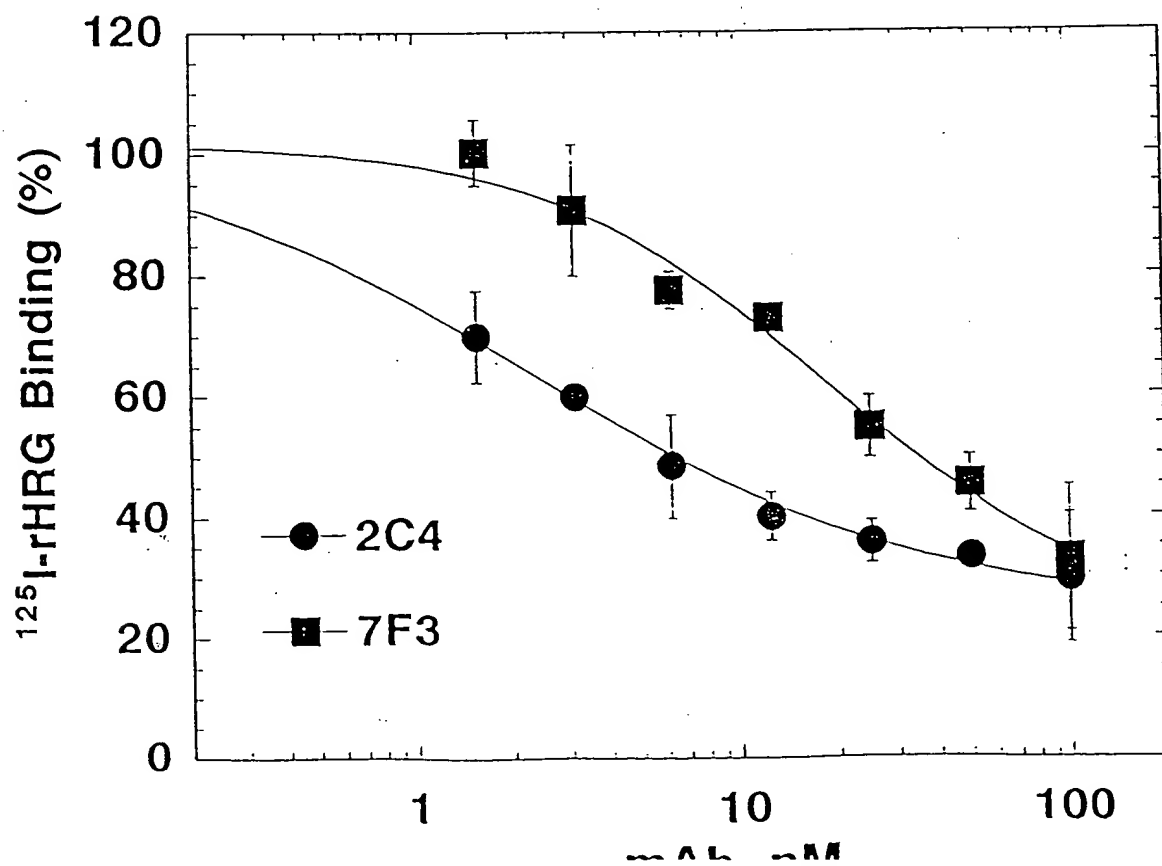


Fig. 2B

000290"00820960

Bound/Total X 100

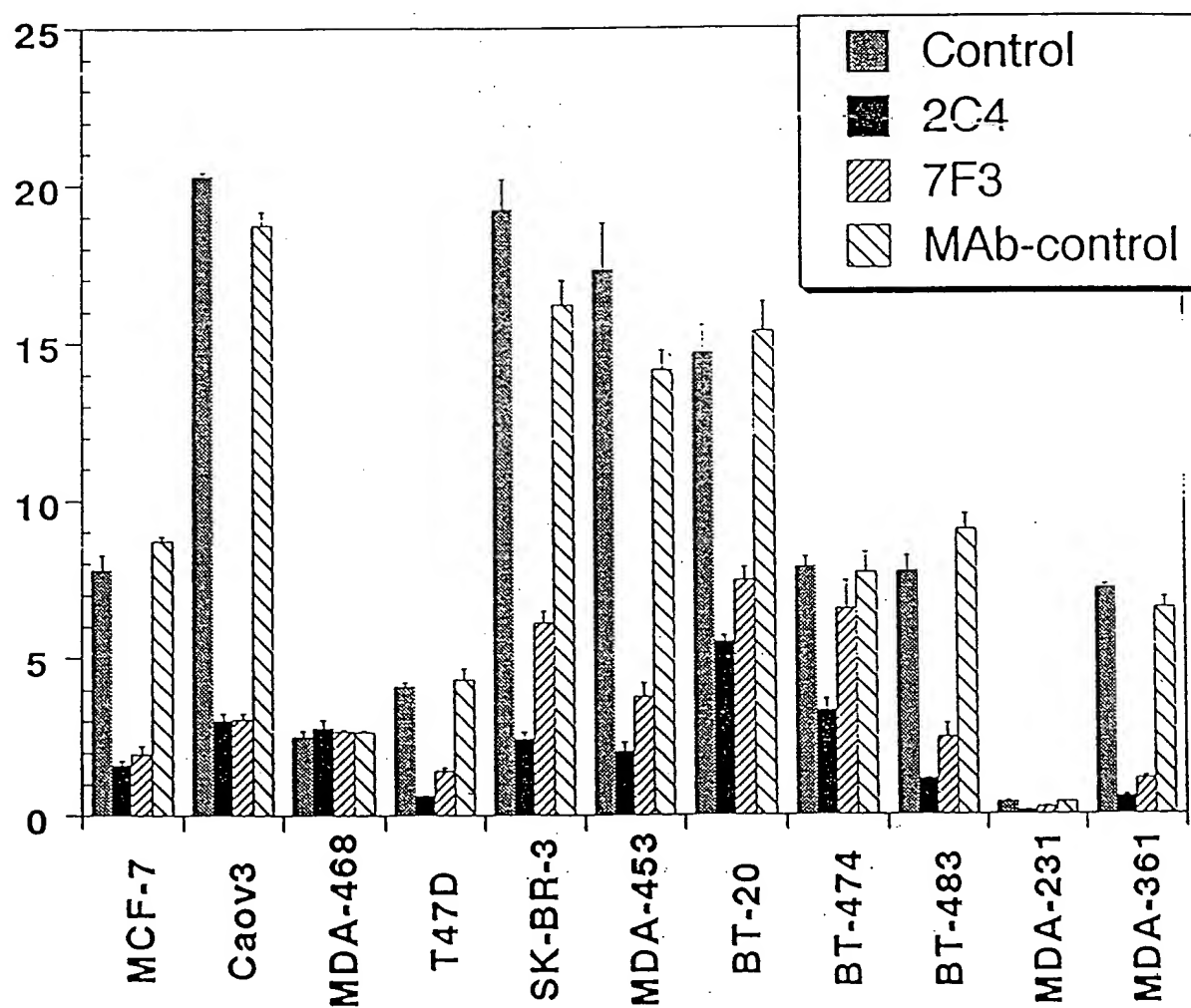


Fig. 3

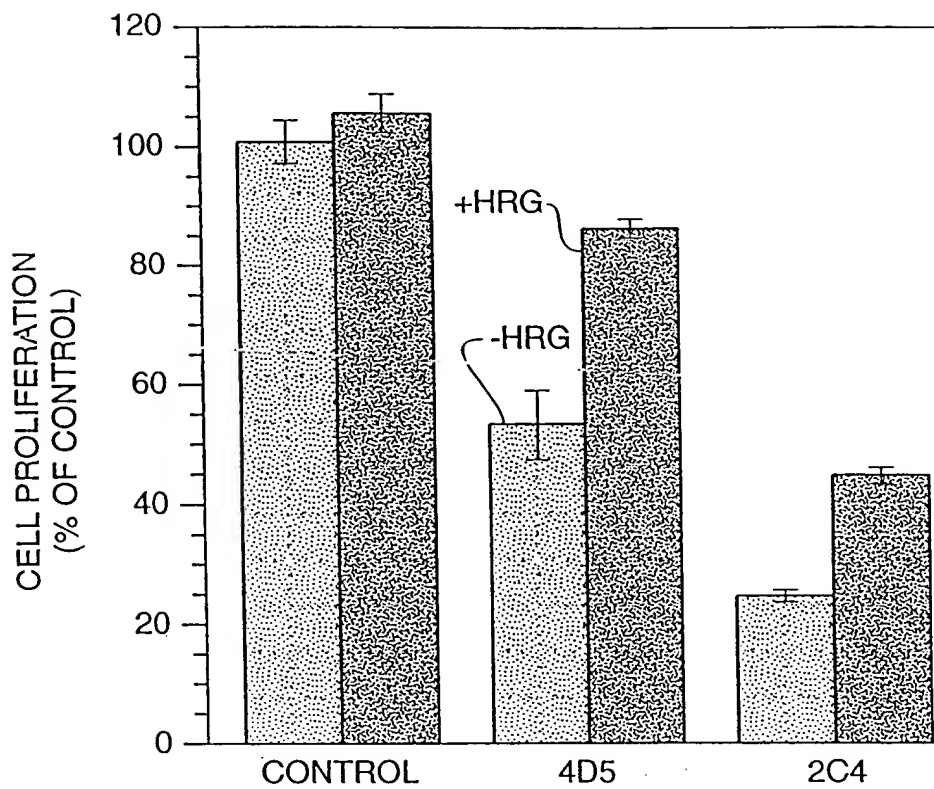


Fig. 4A

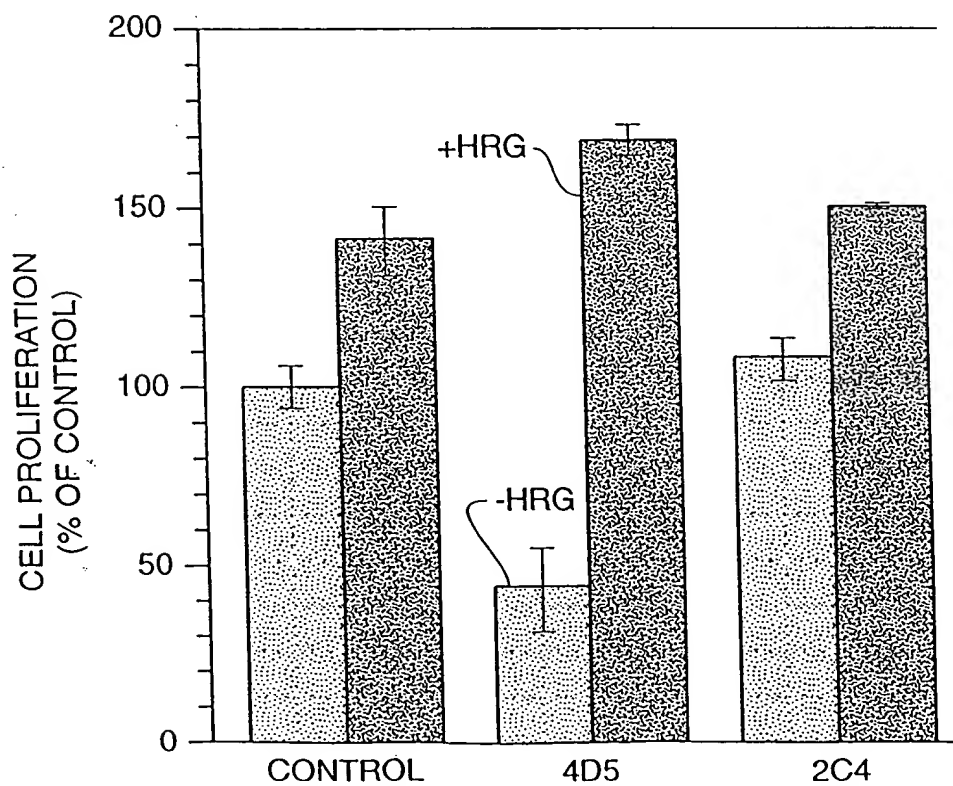


Fig. 4B

Fig. 5A

MCF7  
Low/Normal HER2

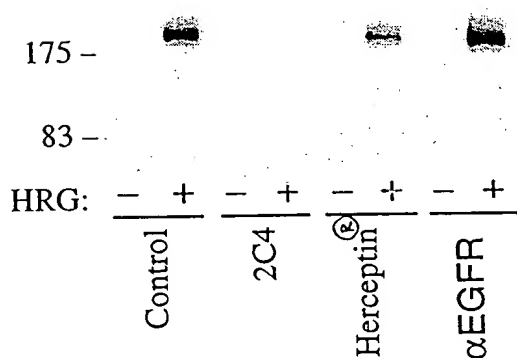
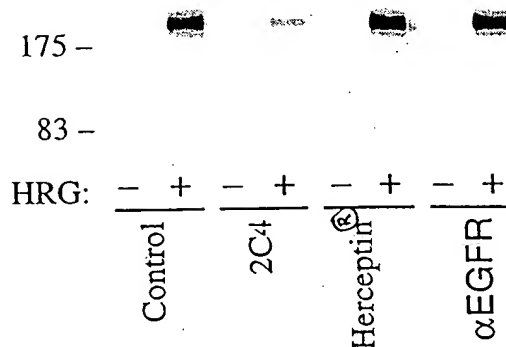


Fig. 5B

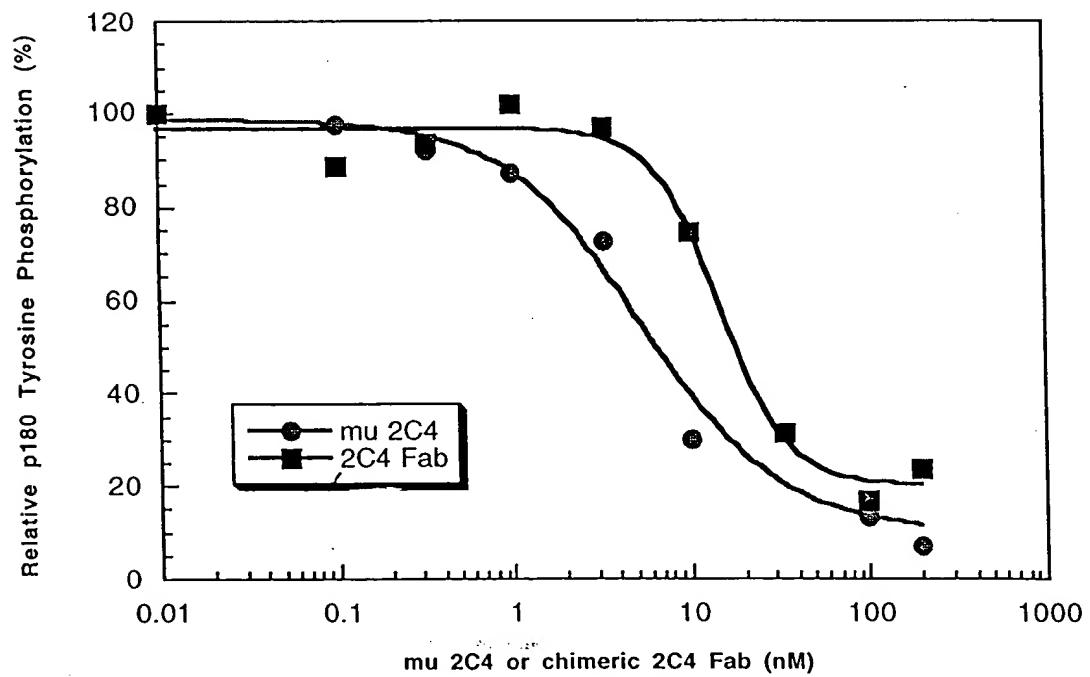
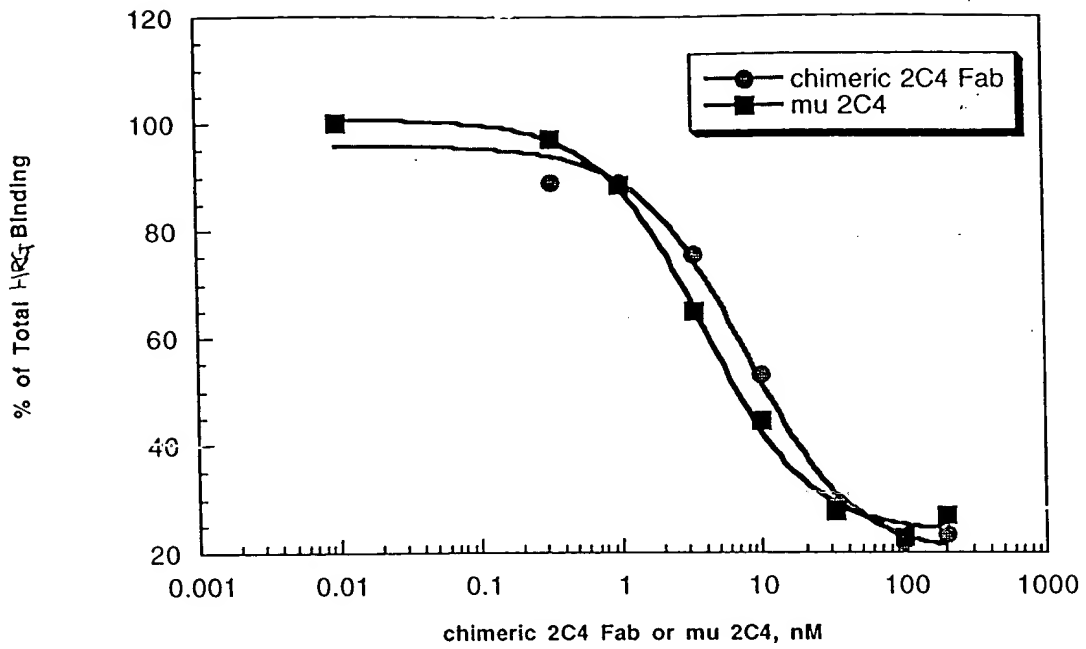
SK-BR-3  
High HER2



IP: αHER2

WB: αHER3

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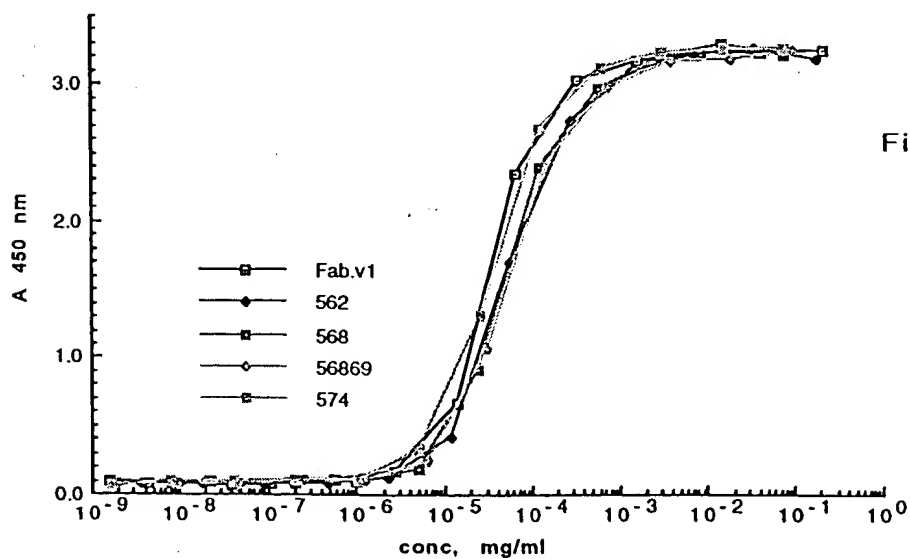
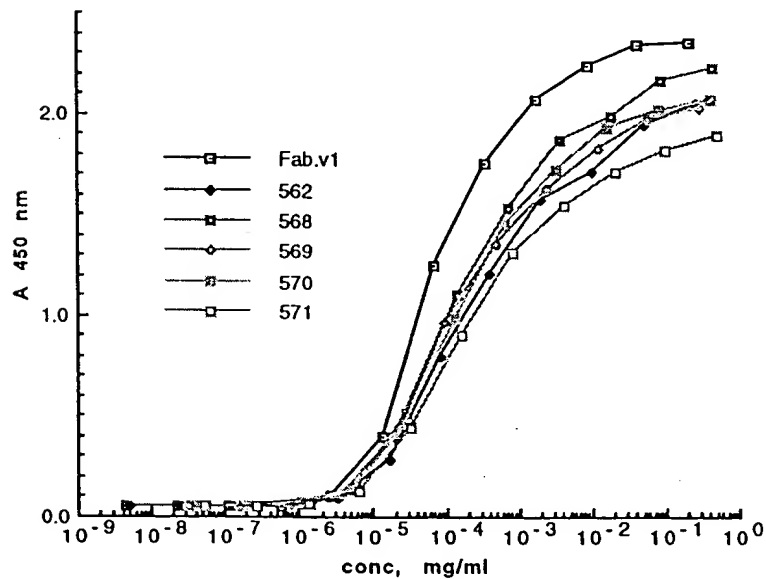
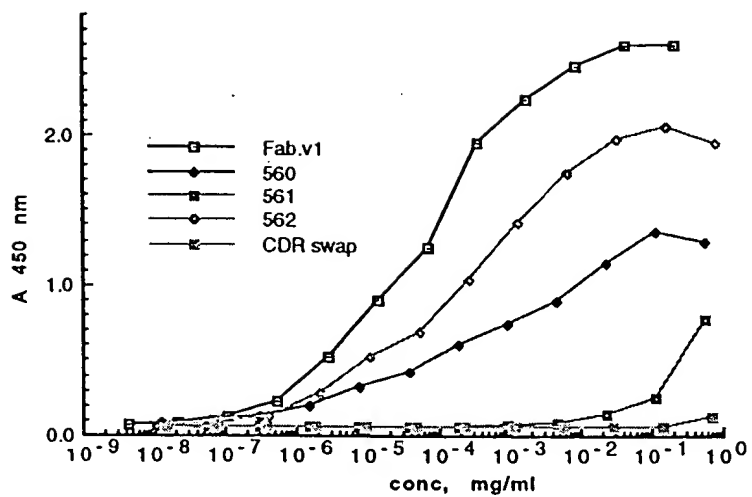


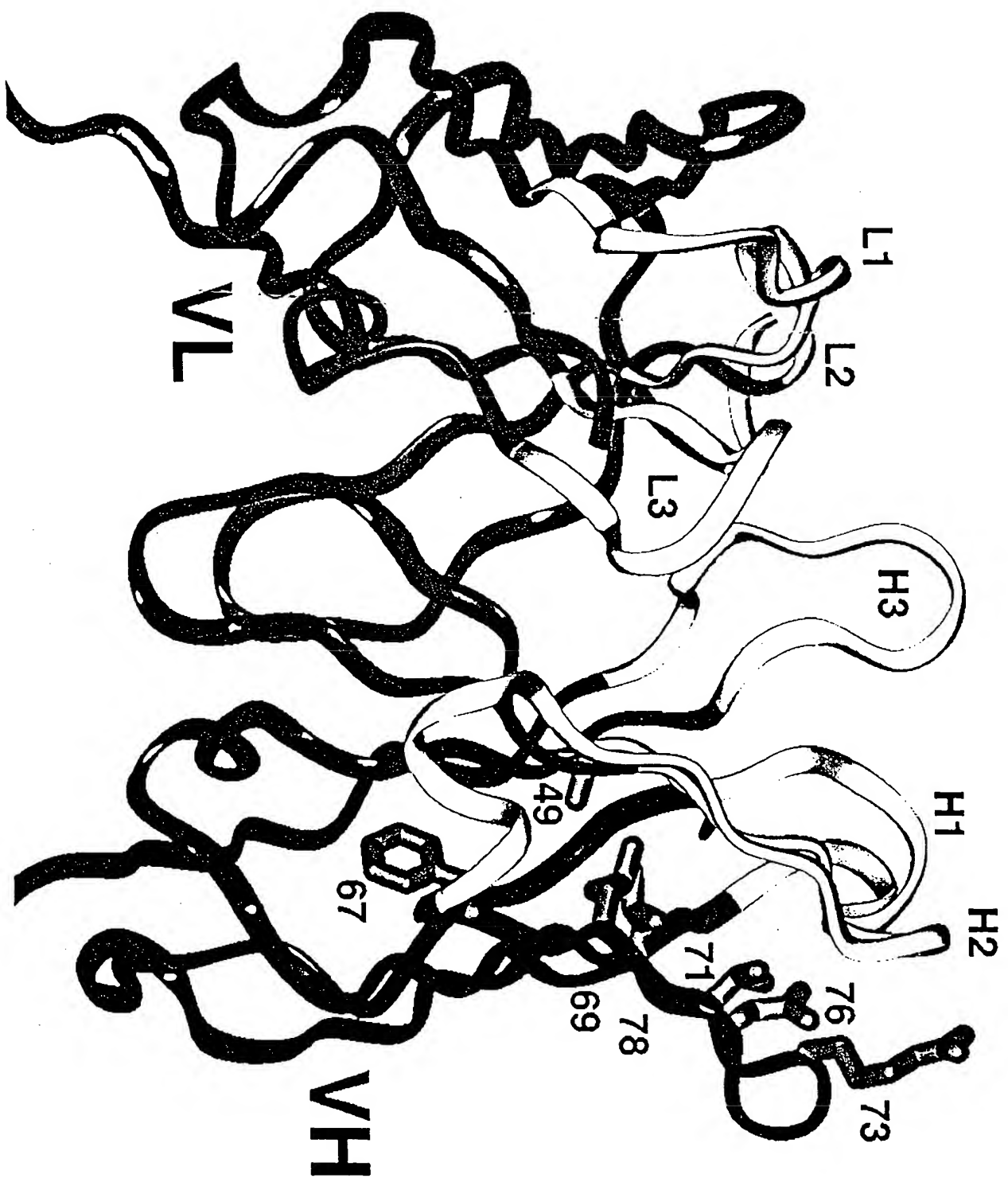
**SECRET**

Fig. 7B: Variable Heavy

		10	20	30	40	
2C4		EVQLQQSGPELVKPGTSVKISCKAS	[GFTFTDYTMD]	WVKQS		
		** ** *	* ** *		* *	
574		EVQLVESGGGLVQPGGSLRLSCAAS	[GFTFTDYTMD]	WVRQA		
			** * *			
hum III		EVQLVESGGGLVQPGGSLRLSCAAS	[GFTFSSYAMS]	WVRQA		
		50 a	60	70	80	
2C4		HGKSLEWIG	[DVNPNSGGSIYNQRFKG]	KASLTVDRSSRIVYM		
		* * **		*** * **** *		
574		PGKGLEWVA	[DVNPNSGGSIYNQRFKG]	RFTLSVDRSKNTLYL		
			***** ** *	* * *		
hum III		PGKGLEWVA	[VISGDGGSTYYADSVKG]	RFTISRDN SKNTLYL		
		abc	90	100ab	110	
2C4		ELRSLTFEDTAVYYCAR	[NLGPSFYFDY]	WGQGTTLTVSS	(SEQ ID NO:2)	
		*** **		**		
574		QMNSLRAEDTAVYYCAR	[NLGPSFYFDY]	WGQGTTLTVSS	(SEQ ID NO:4)	
			*****			
hum III		QMNSLRAEDTAVYYCAR	[GRVGYSLYDY]	WGQGTTLTVSS	(SEQ ID NO:6)	



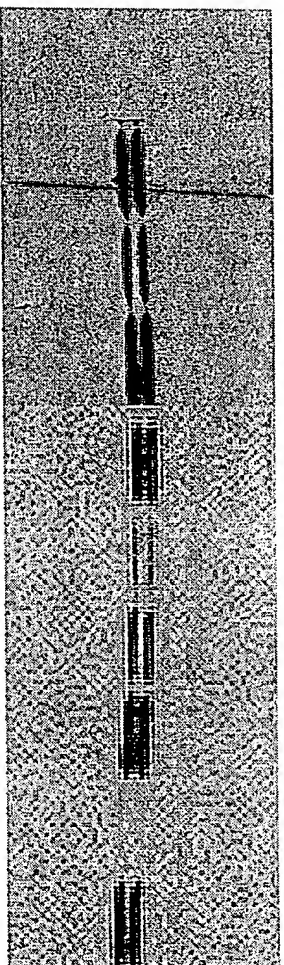




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Fig. 9

Fig. 10



EGF	-	+	+	+	-	-	-	-	-
TGF $\alpha$	-	-	-	-	+	+	+	-	-
HRG	-	-	-	-	-	-	+	+	+
2C4	-	-	+	-	-	+	-	+	-
HERCEPTIN <sup>®</sup>	-	-	-	+	-	-	+	-	+



09602500 00000000

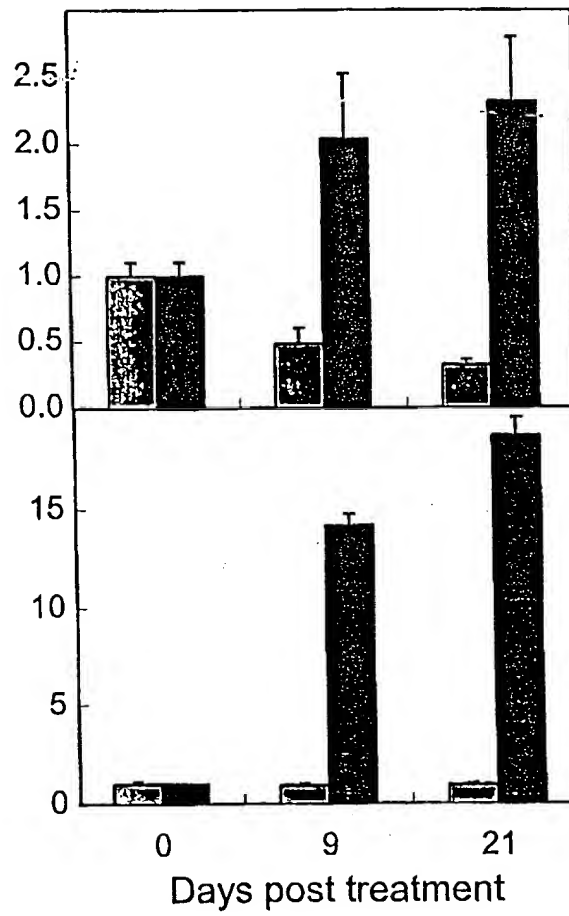


Fig. 12A

**Fig. 12B**

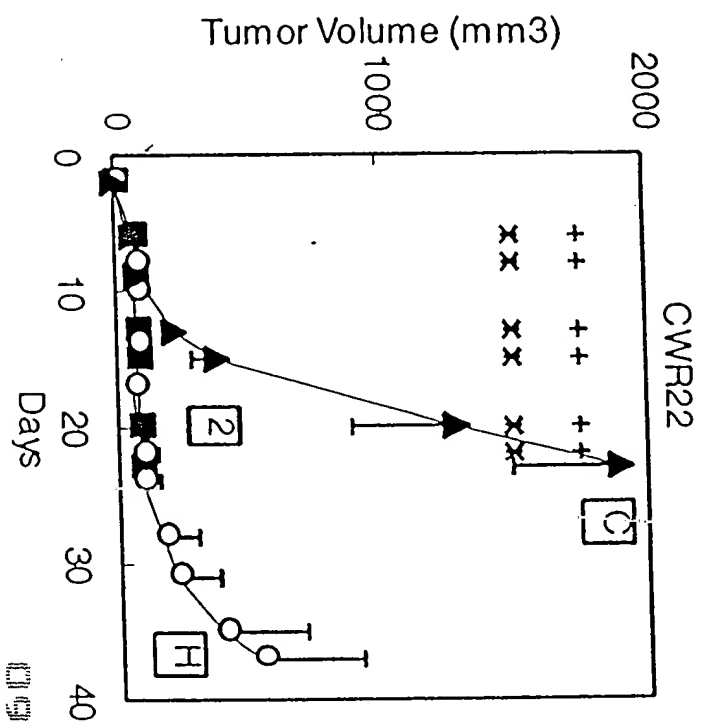


Fig. 13

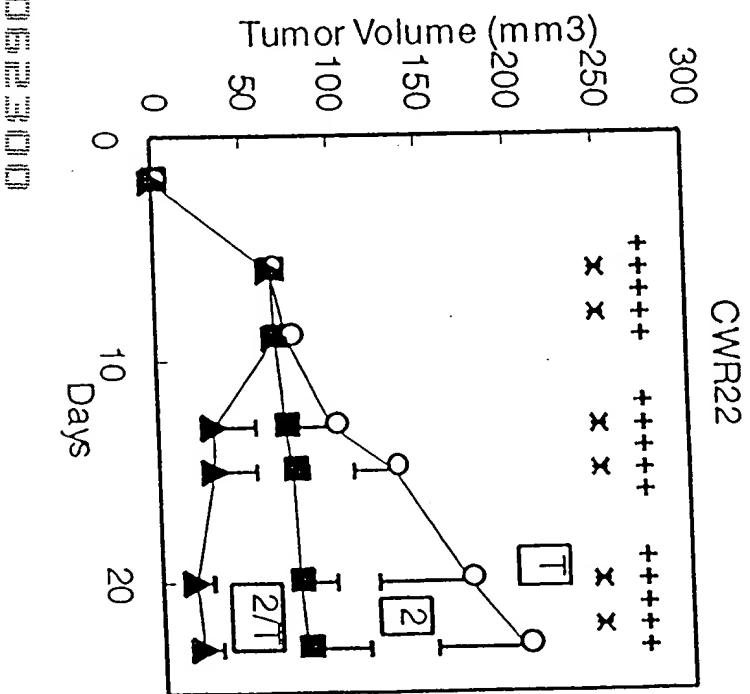


Fig. 14

Fig. 15

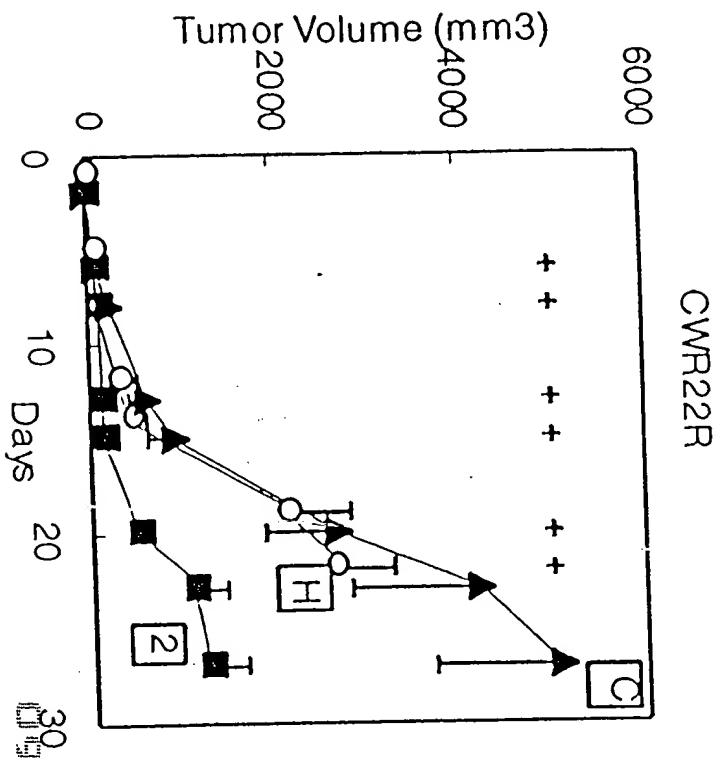


Fig. 16

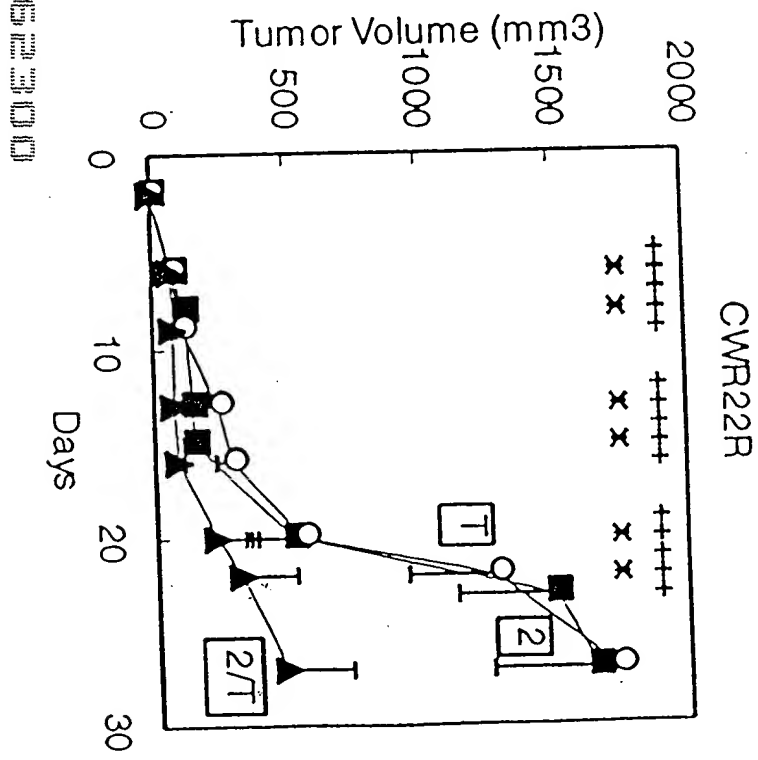


Fig. 17

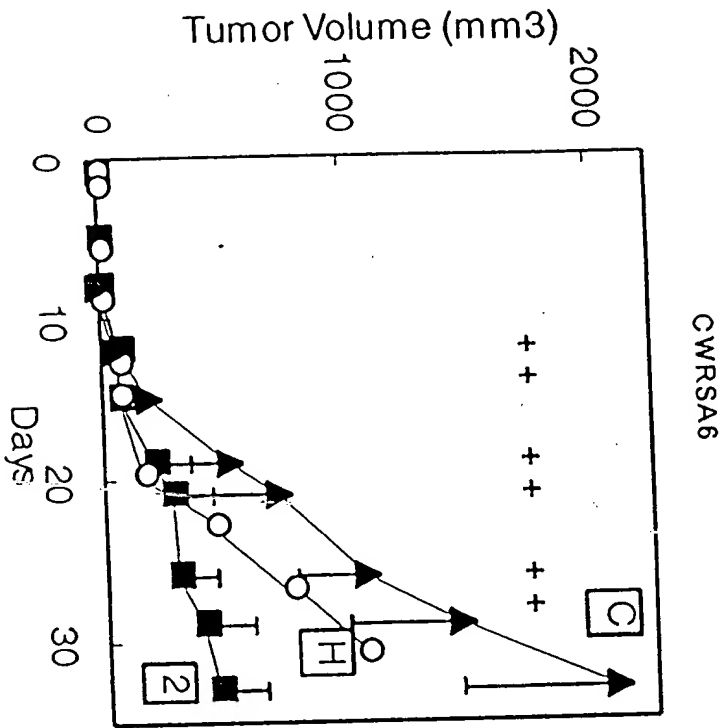
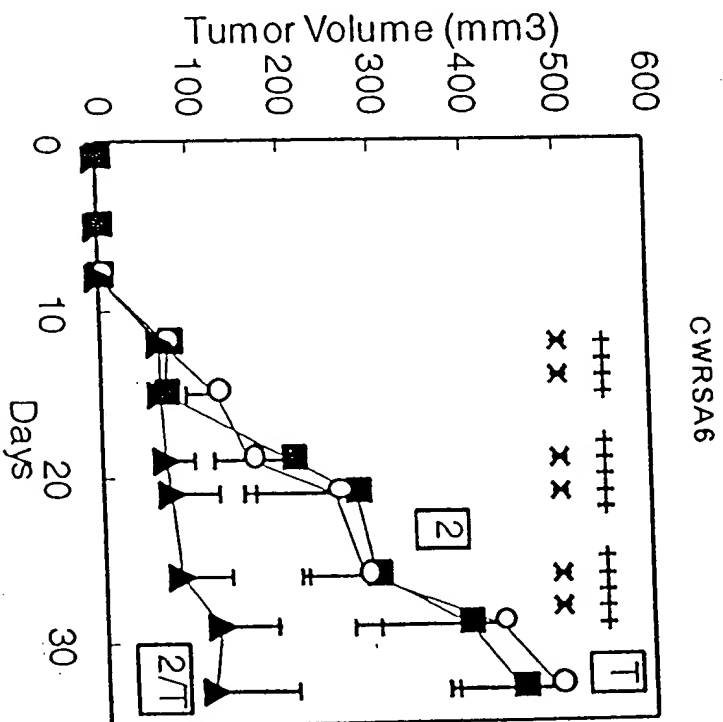


Fig. 18





### Relative TGF- $\alpha$ mRNA Expression

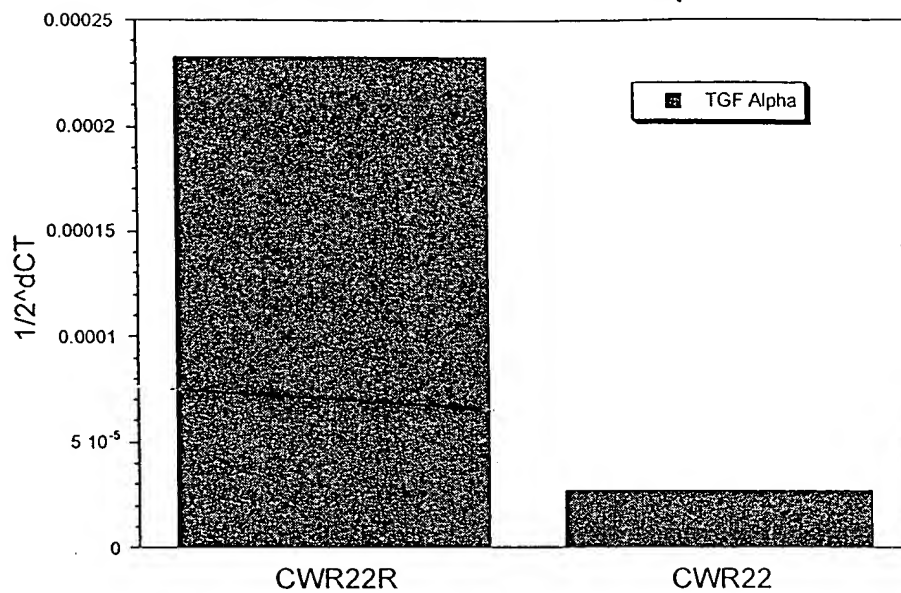


Fig. 19

### Relative HB-EGF mRNA Expression

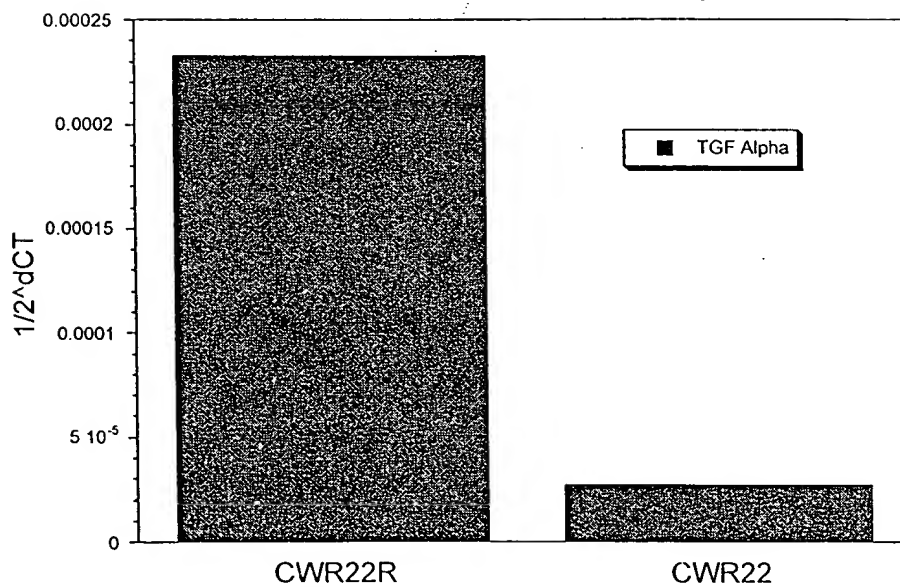
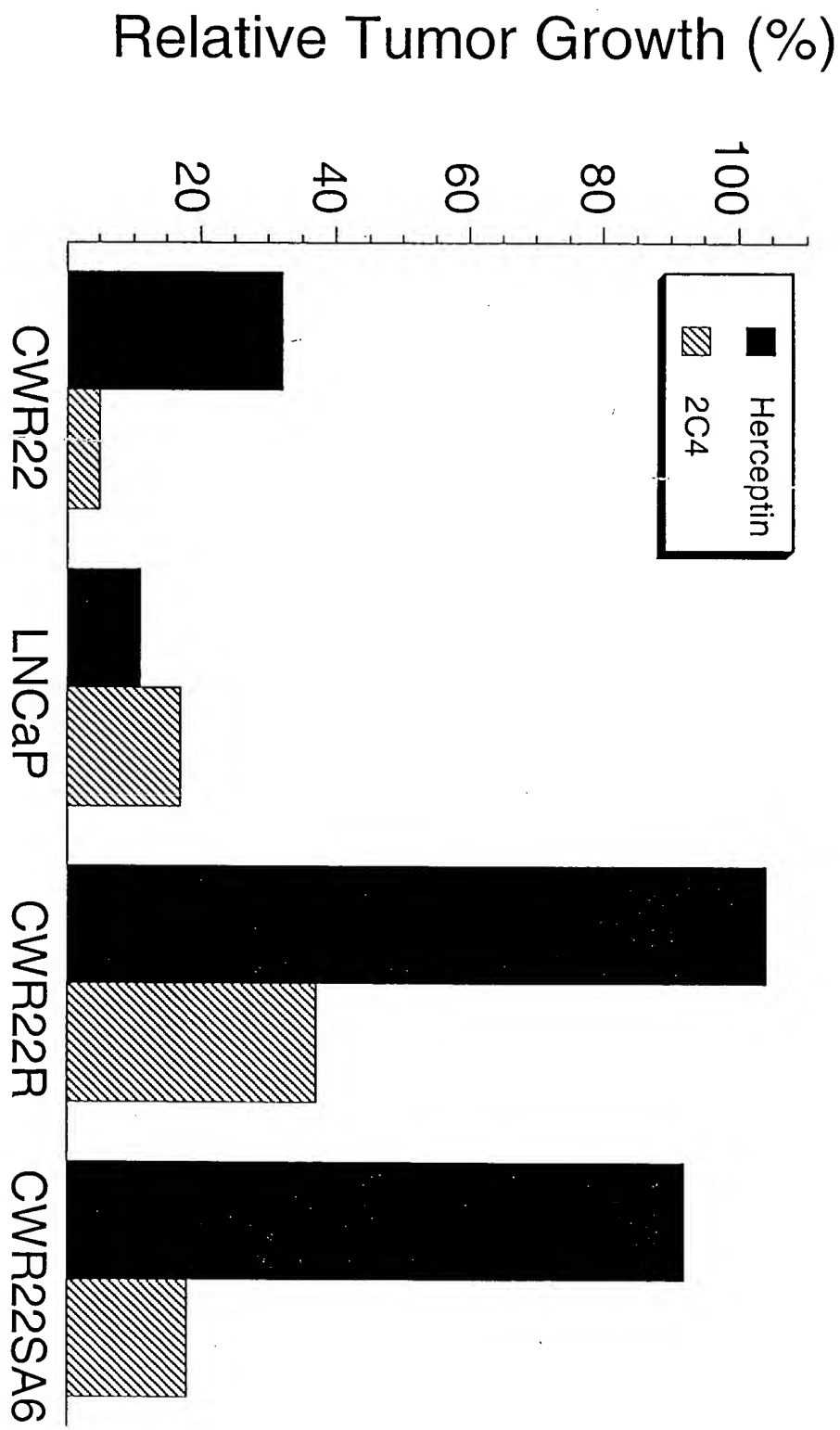


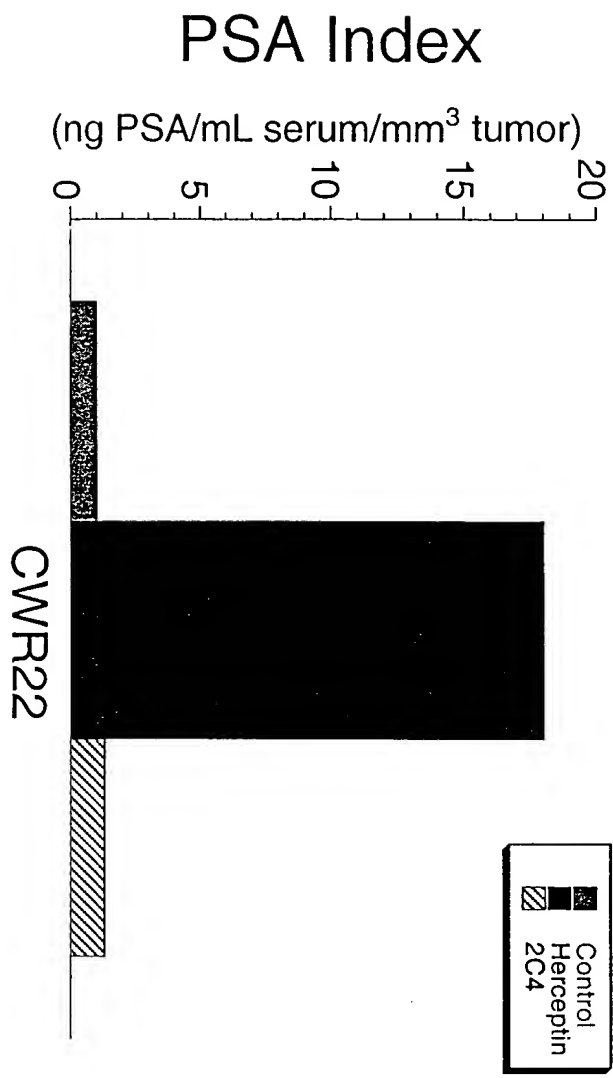
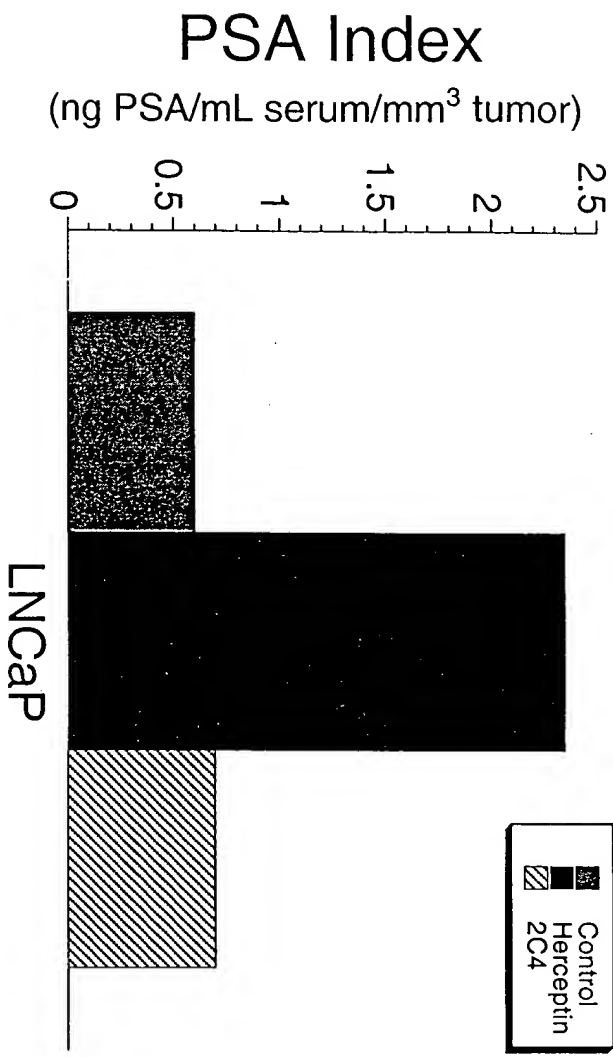
Fig. 20

Fig. 21

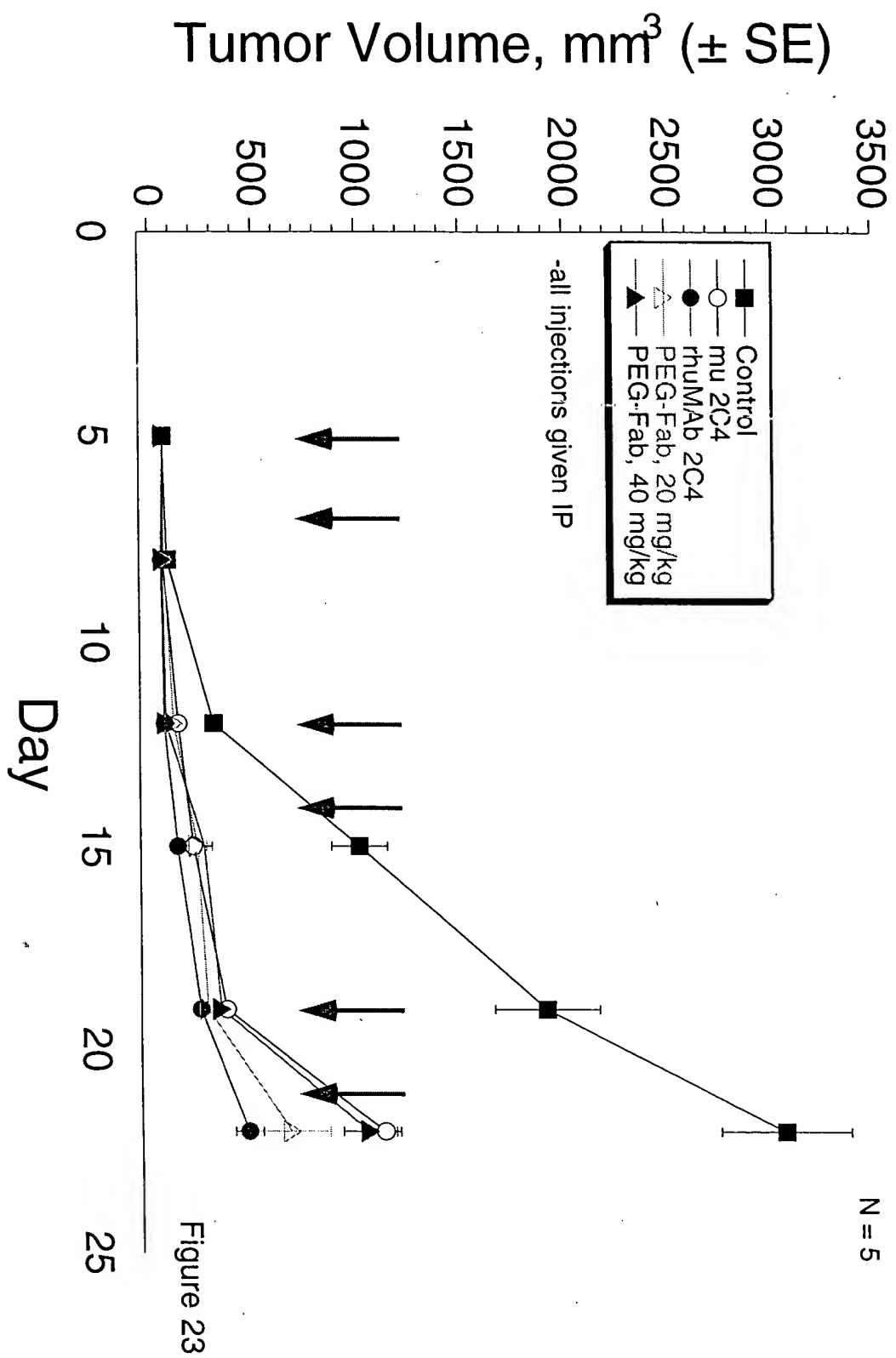


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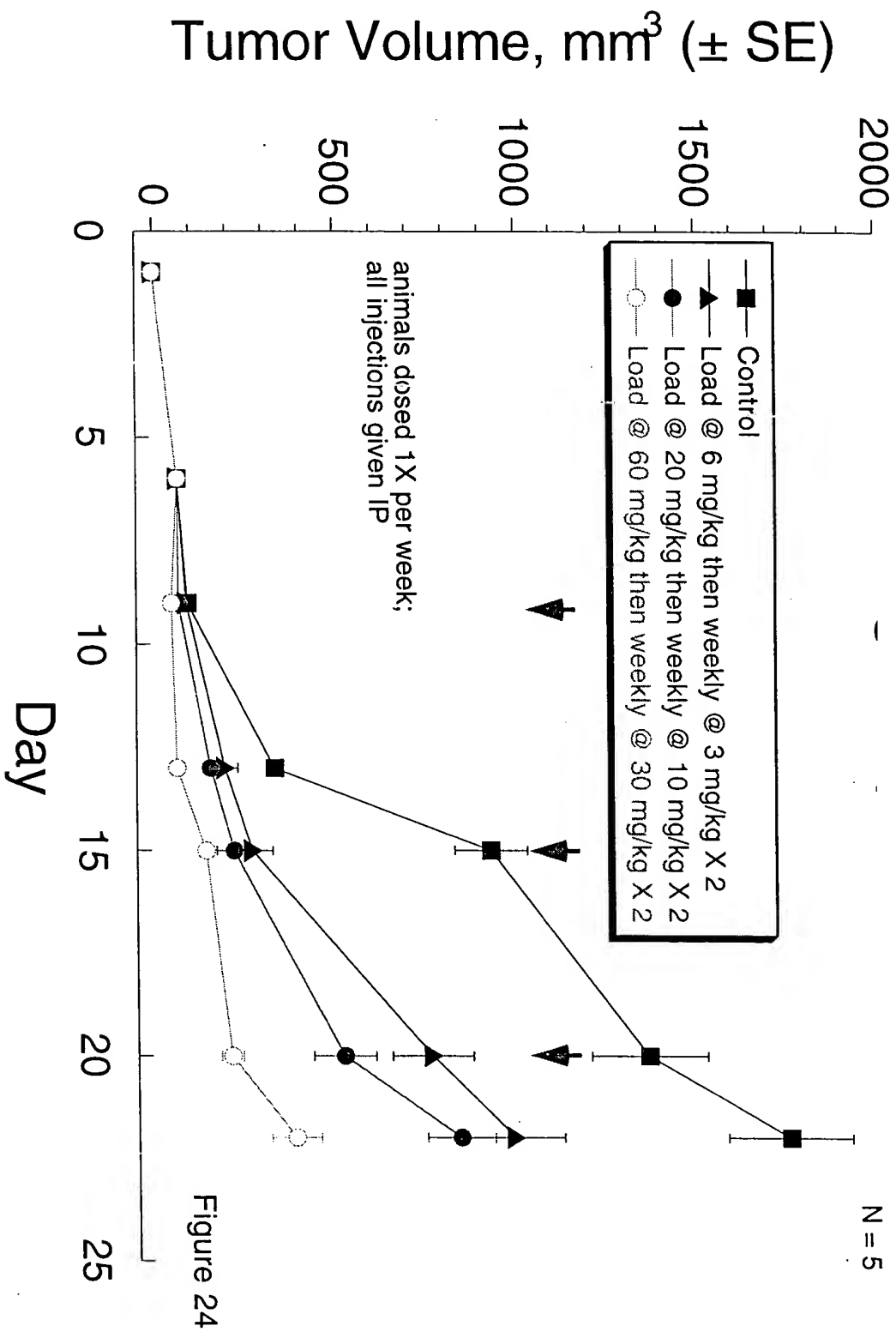
Fig. 2a



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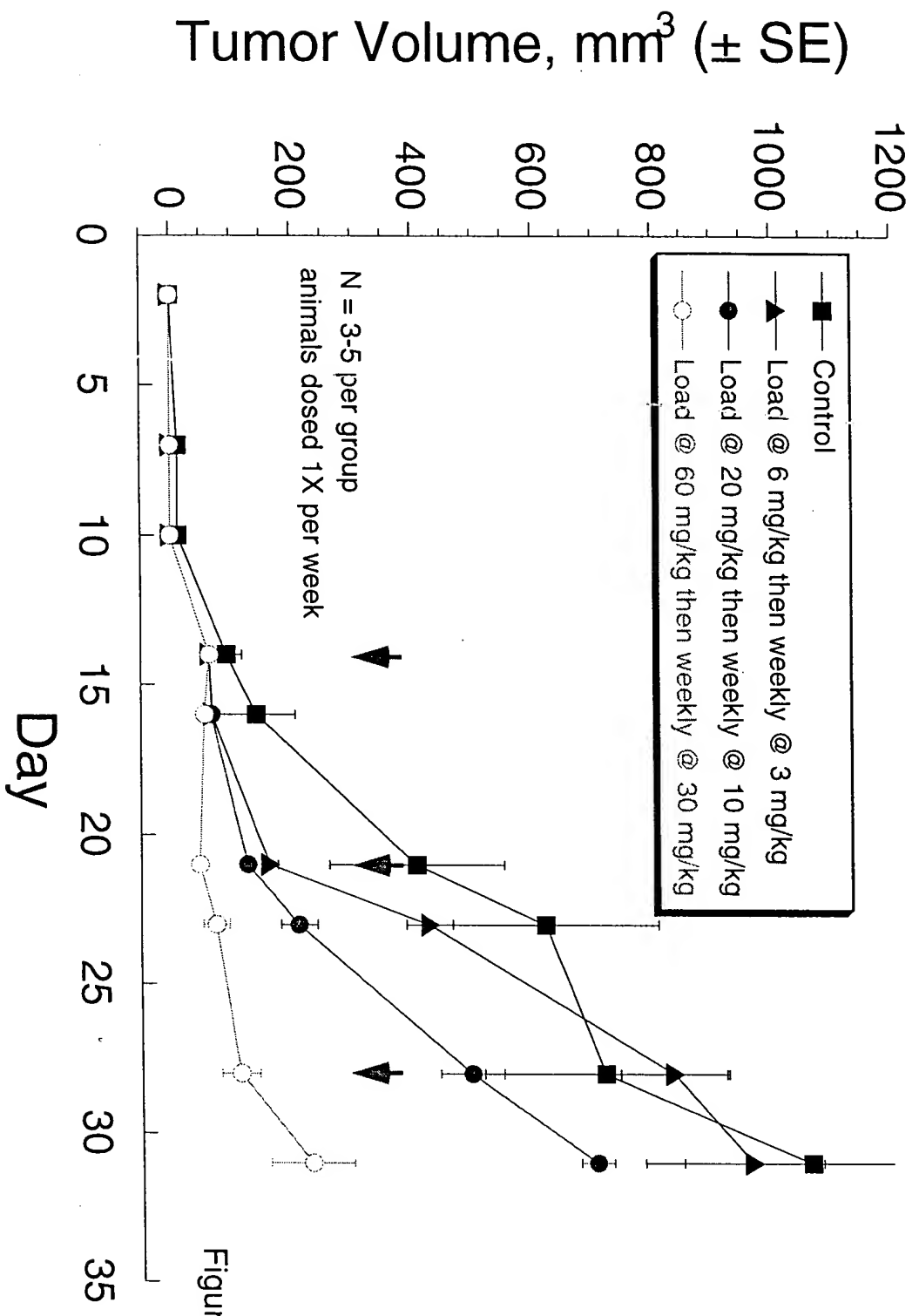
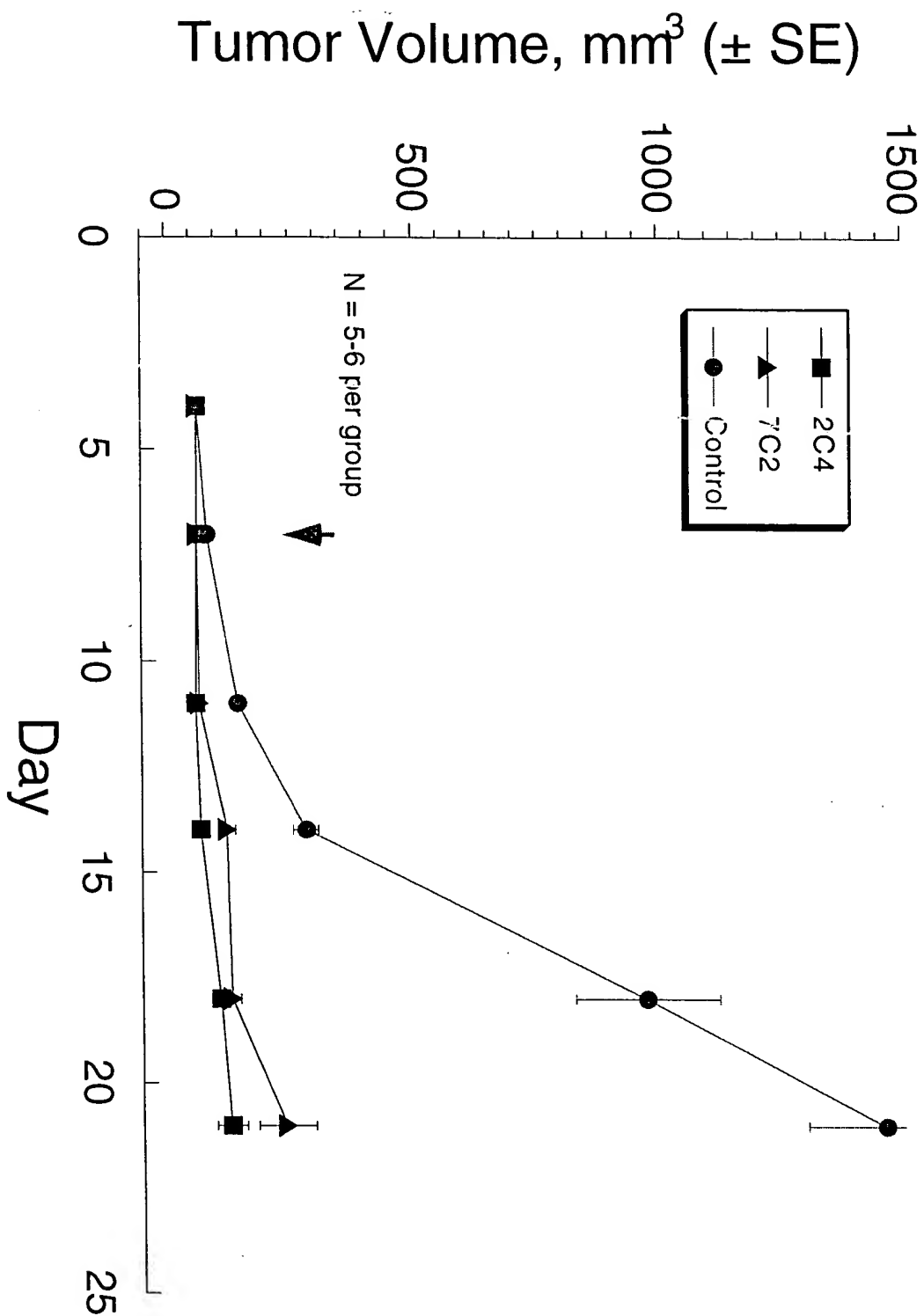


Figure 25

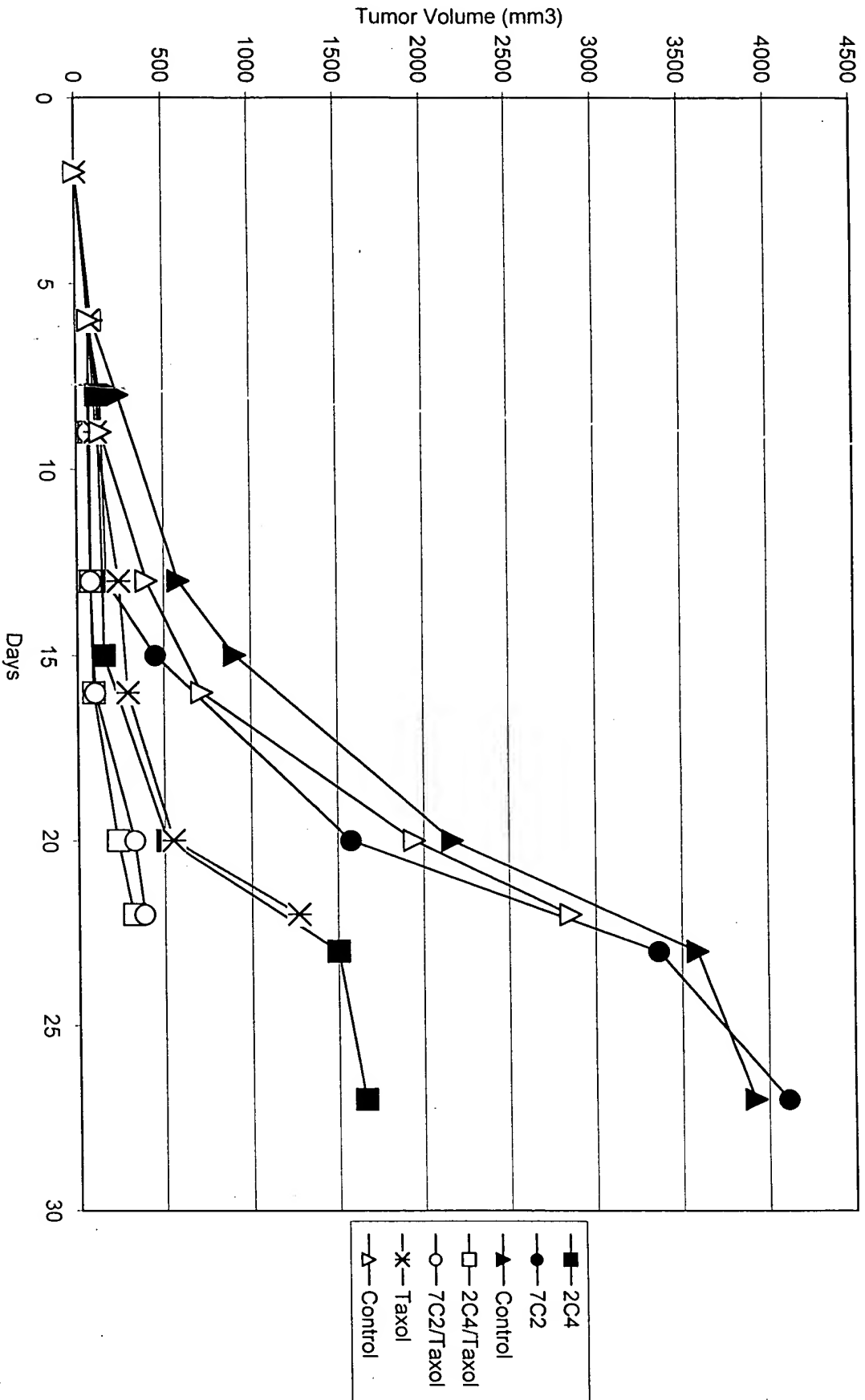
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Fig. 26



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Fig. 27



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